

BIOGRAPHICAL SKETCH

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NAME Thomas Leitner	POSITION TITLE Staff Scientist		
eRA COMMONS USER NAME TKLEITNER			
EDUCATION/TRAINING <i>(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)</i>			
INSTITUTION AND LOCATION	DEGREE <i>(if applicable)</i>	YEAR(s)	FIELD OF STUDY
Royal Institute of Technology, Stockholm, Sweden	B.Sc.	1991	Biochemical Engineering
Karolinska Institute, Stockholm, Sweden	Ph.D.	1996	Virology
Los Alamos National Laboratory, Los Alamos, NM	Postdoc	1996-1998	Theoretical Biology

A. Personal Statement

My expertise rests on that I have studied HIV molecular evolution and molecular epidemiology for 20 years, during which time I've been PI on many projects investigating HIV molecular evolution and computational biology. I have experience from running a Genomics core facility servicing a broad range of pathogen projects. I have published >120 scientific publications, mostly related to computational analyses of HIV evolution and molecular epidemiology, but also other pathogens and the molecular history of the domestic dog. I am currently collaborating with experimental, clinical, and theoretical scientists across the globe. I'm studying HIV evolution within patients, in HIV outbreaks, and in transmission histories. Currently, I'm investigating reconstruction of HIV epidemiology, HIV mother-to-child transmission, new molecular clock approaches, and HIV latency. I'm also involved in analyzing next-generation sequence data to understand sequence diversification in early and chronic infections.

B. Positions and Honors

Positions

1998-2003 Assistant Professor and Head of the HIV & Retrovirus Section at the Swedish Institute for Infectious Disease Control (SMI), Sweden
2001-2003 Head of the Genomics Core facility at the SMI, Sweden
2003-present Staff Scientist at the Los Alamos National Laboratory, Theoretical Biology and Biophysics group, T-6

Honors

1996-1998 Postdoctoral fellowship, Swedish Research Council for Engineering Sciences (TFR)
1998-2002 Research fellowship, Swedish Medical Research Council (MFR)
2005 Outstanding Mentoring Award, LANL
2006 Outstanding Innovation Technology Transfer Award, LANL
2010 Outstanding Innovation Technology Transfer Award, LANL
2014 Postdoc Distinguished Mentor Award, LANL

Other Experience

1998-present Advisor for 9 postdocs, 11 graduate students, and other students
2003-2007 Chief editor of the HIV sequence database
2005-2008 Team leader HIV databases team, T-10, Los Alamos National Laboratory
2004-present Organizing committee, HIV Dynamics & Evolution conference
2009-present Affiliate at Center of Nonlinear Studies (CNLS), Los Alamos National Laboratory
2010-present NIH *ad-hoc* reviewer at several study sections
2010-2012 Guest Associate Editor PLoS Computational Biology
2014-present Associate Editor Molecular Biology & Evolution

C. Selected peer-reviewed publications (in chronological order)

- Scarlatti G, **Leitner T**, Halapi E, Wahlberg J, Marchisio P, Clerici-Schoeller MA, Wigzell H, Fenyö EM, Albert J, Uhlén M, Rossi P. 1993. Comparison of variable region 3 sequences of human immunodeficiency virus type 1 from infected children with the RNA and DNA sequences of the virus populations of their mothers. PNAS USA 90:1721-1725
- Leitner T**, Halapi E, Scarlatti G, Rossi P, Albert J, Fenyö EM, Uhlén M. 1993. Analysis of heterogeneous viral populations by direct DNA sequencing. BioTechniques 15:120-126.
- Pettersson B, **Leitner T**, Ronaghi M, Bölske G, Uhlén M, Johansson KE. 1996. The phylogeny of the *Mycoplasma mycoides* cluster as determined by sequence analysis of the 16S rRNA genes from two rRNA operons. J Bact 178: 4131-4142.
- Leitner T**, Escanilla D, Franzén C, Uhlén M, Albert J. 1996. Accurate reconstruction of a known HIV-1 transmission history by phylogenetic tree analysis. PNAS USA 93:10864-10869.
- Leitner T**, Kumar S, Albert J. 1997. Tempo and mode of nucleotide substitutions in gag and env gene fragments in human immunodeficiency virus type 1 populations with a known transmission history. J Virol 71:4761-4770
- Halapi E, **Leitner T**, Jansson M, Scarlatti G, Orlandi P, Plebani A, Romiti L, Albert J, Wigzell H, Rossi P. 1997. Correlation between HIV sequence evolution, specific immune response and clinical outcome in vertically infected infants. AIDS 11:1709-1717.
- Alaeus A, **Leitner T**, Lidman K, Albert J. 1997. Most genetic subtypes of HIV-1 have entered Sweden. AIDS 11:199-202.
- Nijhuis M, Boucher CAB, Schipper P, **Leitner T**, Schuurman R, Albert J. 1998. Stochastic processes strongly influence HIV-1 evolution during suboptimal protease-inhibitor therapy. PNAS USA 95:14441-14446.
- Leitner T**, Albert J. 1999. The molecular clock of HIV-1 unveiled through analysis of a known transmission history. PNAS USA 96:10752-10757.
- Robertson DL, Anderson JP, Bradac JA, Carr JK, Foley B, Gao F, Hahn BH, Kuiken C, Learn GH, **Leitner T**, McCutchan F, Osmanov S, Peeters M, Pieniazek D, Salminen M, Wolinsky S, Korber B. 2000. HIV-1 nomenclature proposal. Science 288:55-57.
- Leitner T**, Albert J. 2000. Reconstruction of HIV-1 transmission chains for forensic purposes. AIDS Rev. 2:241-251.
- Savolainen P, Zhang Y-P, Luo J, Lundeberg J, **Leitner T**. 2002. Genetic evidence for an East Asian origin of domestic dogs. Science 298:1610-1613.
- Wilbe K, Salminen MO, Laukkanen T, McCutchan F, Ray SC, Albert J, **Leitner T**. 2003. Investigation of novel HIV-1 recombinant forms using the branching index. Virology 316:116-125.
- Savolainen P, **Leitner T**, Wilton AN, Matisoo-Smith E, Lundeberg J. 2004. A detailed picture of the origin of the Australian dingo, obtained from the study of mitochondrial DNA. PNAS USA 101:12387-12390.
- Zuniga R, Lucchetti A, Galvan P, Sanchez S, Sanchez C, Hernandez A, Sanchez H, Frahm N, Linde CH, Hewitt HS, Hildebrand W, Altfeld M, Allen TM, Walker BD, Korber TM, **Leitner T**, Brander C. 2006. Relative dominance of gag p24-specific cytotoxic T lymphocytes is associated with human immunodeficiency virus control. J Virol 80: 3122-3125.
- Schultz A-K, Zhang M, **Leitner T**, Kuiken C, Korber B, Morgenstern B, Stanke M. 2006. Jumping profile Hidden Markov Models for database searching and applications to recombination sites in HIV and HCV genomes. BMC Bioinf 7: 265-280.
- Zhang M, Schultz A-K, Calef C, **Leitner T**, Korber B, Morgenstern B, Stanke M. 2006. jpHMM at GOBICS: a web server to detect genomic recombination in HIV. Nucleic Acids Res 34: W463-W465.
- Leitner T**, Dazza M-C, Ekwilanga M, Apetrei C, Saragosti S. 2007. Sequence diversity among chimpanzee simian immunodeficiency viruses (SIVcpz) suggests that SIVcpzPtt was derived from SIVcpzPtt through additional recombination events. AIDS Res Hum Retrovirus 23: 1114-1118.
- Maljkovic Berry I, Ribeiro R, Kothari M, Athreya G, Daniels M, Lee HY, Bruno W, **Leitner T**. 2007. Unequal evolutionary rates in the HIV-1 pandemic: The evolutionary rate of HIV-1 slows down when the epidemic rate increases. J Virol 81: 10625-10635.
- Skar H, Sylvan S, Hansson H-B, Gustavsson O, Boman H, Albert J, **Leitner T**. 2008. Multiple HIV-1 introductions into the Swedish intravenous drug user population in the years of 2001-2002. Genetics, Infection and Evolution 8: 545-552.

- Hraber P, Kuiken C, Waugh M, Geer S, Bruno WJ, **Leitner T**. 2008. Automatic classification of HCV and HIV-1 sequences with the branching index. *J Gen Virol* 89: 2098-2107
- Lee HY, Park S, Perelson AS, **Leitner T**. 2008. Dynamic correlation between intrahost HIV-1 quasispecies evolution and disease progression. *PLoS Comput Biol* 4: e1000240.
- Schultz A-K, Zhang M, Bulla I, **Leitner T**, Korber B, Morgenstern B, Stanke M. 2009. jpHMM: Improving the reliability of recombination prediction in HIV-1. *Nucleic Acids Res* 37: W647-651.
- Tsibris AMN, Korber B, Arnaout R, Russ C, Lo C-C, **Leitner T**, Gaschen B, Theiler J, Paredes R, Su Z, Hughes MD, Gulick R, Greaves, Coakley E, Flexner C, Nusbaum C, Kuritzkes DR. 2009. Quantitative deep sequencing reveals dynamic HIV-1 escape and large population shifts during CCR5 antagonist therapy *in vivo*. *PLoS One* 4: e5683.
- Pang J, Kluetsch C, Zou X-J, Zhang A-B, Lou L-Y, Angleby H, Ardalan A, Ekstrom C, Skollermo A, Lundeberg J, Matsumura A, **Leitner T**, Zhang Y-P, Savolainen P. 2009. The dog originated south of Yangtze River less than 16,000 years ago, from numerous wolves. *Mol Biol Evol* 26: 2849-2864.
- Maljkovic Berry I, Athreya G, Kothari M, Daniels M, Korber B, Kuiken C, **Leitner T**. 2009. The evolutionary rate dynamically tracks changes in HIV-1 epidemics: application of a simple method for optimizing the evolutionary rate in phylogenetic trees with longitudinal data. *Epidemics* 1: 230-239.
- Neher RA, **Leitner T**. 2010. Recombination rate and selection strength in HIV intra-patient evolution. *PLoS Comput Biol* 6: e1000660.
- Zhang M, Macke J, Foley B, Schultz A-K, Morgenstern B, Korber B, **Leitner T**. 2010. The role of recombination in the emergence of a complex and dynamic HIV epidemic. *Retrovirology* 7:25.
- Hedskog C, Mild M, Jernberg J, Sherwood E, Bratt G, **Leitner T**, Lundeberg J, Andersson B, Albert J. 2010. Dynamics of HIV-1 quasispecies during antiviral treatment dissected using ultra-deep pyrosequencing. *PLoS One* 5(7): e11345.
- Skar H, Borrego P, Wallstrom TC, Mild M, Marcelino J, Barroso H, Taveira N, **Leitner T**, Albert J. 2010. HIV-2 genetic evolution in patients with advanced disease is faster than in matched HIV-1 patients. *J Virol* 84: 7412-7415.
- Fischer W, Bhattacharya T, Keele B, Giorgi E, Hraber P, Ganusov V, Lo C-C, **Leitner T**, Nag A, Wallstrom T, Han C, Gleasner C, Green L, Wang S, McMichael A, Haynes B, Hahn B, Perelson A, Borrow P, Shaw G, Korber B. 2010. Rapid mutational escape from cytotoxic T-cell responses in acute HIV-1 infection – an ultra-deep view. *PLoS One* 5(8): e12303.
- Skar H, Axelsson M, Liitsola K, Brummer-Korvenkontio H, Thalme A, Gyllenstein K, Berggren I, **Leitner T**, Albert J. 2011. The dynamics of two separate but linked CRF01_AE outbreaks among IDUs in Stockholm and Helsinki. *J Virol* 85: 510-518.
- Cale EM, Hraber P, Giorgi EE, Fischer W, Bhattacharya T, **Leitner T**, Yeh WW, Gleasner C, Green LD, Han CS, Korber B, Letvin NL. 2011. CD8+ T lymphocytes recognize but fail to contain the accumulation of SIV epitope escape mutations. *J Virol* 85:3746-3757.
- Skar H, Gutenkunst RN, Wilbe K, Alaeus A, Albert J, **Leitner T**. 2011. Daily sampling of an HIV-1 patient with slowly progressing disease displays persistence of multiple env subpopulations consistent with neutrality. *PLoS One* 6(8): e21747.
- Desmarais SM, **Leitner T**, Barron AE. 2012. Quantitative experimental determination of primer-dimer formation risk by free-solution conjugate electrophoresis. *Electrophoresis* 33(3): 483-491.
- Graw F, **Leitner T**, Ribeiro RM. 2012. Agent-based and phylogenetic analyses reveal how HIV-1 moves between risk groups: injecting drug users sustain the heterosexual epidemic in Latvia. *Epidemics* 4(2):104-116.
- Immonen T, Gibson R, **Leitner T**, Arts EJ, Somersalo E, Calvetti D. 2012. A hybrid stochastic-deterministic computational model accurately describes spatial dynamics and virus diffusion in HIV-1 growth competition assay. *J Theor Biol* 17(312C): 120-132.
- Skar H, Albert J, **Leitner T**. 2013. Towards estimation of HIV-1 date of infection: A time-continuous IgG-model shows that seroconversion does not occur at the midpoint between negative and positive tests. *PLoS One* 8(4): e60906.
- Brodin J, Krishnamoorthy M, Athreya G, Fischer W, Hraber P, Gleasner C, Green L, Korber K, **Leitner T**. 2013. A multiple-alignment based primer design algorithm for genetically variable DNA targets. *BMC Bioinformatics* 14:255.
- Romero-Severson E, Skar H, Bulla I, Albert J, **Leitner T**. Timing and order of transmission events is not directly reflected in a pathogen phylogeny. 2014. *Mol Biol Evol* 31(9): 2472-2482.

Immonen TT, **Leitner T**. Reduced evolutionary rates in HIV-1 reveal extensive latency periods among replicating lineages. 2014. *Retrovirology* 11(1):81.

Yoon H, **Leitner T**. PrimerDesign-M: a multiple-alignment based multiple-primer design tool for walking across variable genomes. 2015. *Bioinformatics* 31(9):1472-1474.

Romero-Severson EO, Petrie CL, Ionides E, Albert J, **Leitner T**. 2015. Trends of HIV-1 incidence with credible intervals in Sweden 2002-2009 reconstructed using a dynamic model of within-patient IgG growth. *Int J Epidemiol* 44:998-1006.

Romero-Severson EO, Volz E, Koopman JS, **Leitner T**, Ionides EL. 2015. Dynamic variation in sexual contact rates for a cohort of HIV-negative gay men. *Am J Epidemiol* 182:255-262.

D. Research Support

Ongoing Research Support

R01AI087520 NIH/NIAID Reconstructing HIV Epidemics from HIV Phylogenetics The overall goal with this project is to create realistic models connecting HIV sequence evolution within a host to how HIV spreads among hosts, i.e., the epidemic dynamics in the host population. Role: PI, study design, phylogenetics, modeling	(Leitner)	12/01/2009 – 03/31/2020
236617 UC Lab Research Program Accurate evolutionary rates for precise pathogen sourcing The overall goal with this project is to create more realistic molecular clocks to understand virus evolution. Role: PI, phylogenetics, modeling	(Leitner)	07/01/2012 – 09/18/2015
R01AI097265 NIH/NIAID HIV-1 Evolution and Functional Correlates of MTCT The overall goal with this project is to understand biological and genetic determinants of HIV mother-to-child transmission. Role: Co-investigator, study design, phylogenetics, modeling	(Luzuriaga, Janoff)	04/01/2012 – 03/31/2017
AI2013183 NIH/NIAID HIV/SIV Database and analysis unit The overall goal with this project is to provide the international scientific community with a richly annotated HIV database of DNA sequences and immunological information and creating user-friendly bioinformatics tools. Role: Co-investigator, bioinformatics development, sequence alignments and scientific content	(Korber)	12/15/2014 – 12/14/2021

Completed Research Support in last 3 years

R21AI106437 NIH/NIAID Quantifying The Effect Of HIV Latency The goal with this project is to quantify and model HIV latency using sequence and clinical data. Role: PI, phylogenetics, modeling	(Leitner)	07/01/2013 – 05/31/2015
NIH-DOE contract Y1-AI-8309 NIH/NIAID HIV/SIV Database and analysis unit The overall goal with this project is to provide the international scientific community with a richly annotated HIV database of DNA sequences and immunological information and creating user-friendly bioinformatics tools. Role: Co-PI, bioinformatics development, sequence database scientific content	(Korber, Kuiken, Leitner)	12/14/2007 – 12/14/2014